



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/691,165

DATE: 09/14/2004

TIME: 10:19:31

Input Set : A:\CURA 85 CON Sequence Listing 08\_30\_2004

Output Set: N:\CRF4\09142004\J691165.raw

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3 <110> APPLICANT: Prayaga, Sudhirdas K
4   Taupier Jr, Raymond J
5   Bandaru, Raj
7 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAME
9 <130> FILE REFERENCE: Cura 85 CON
11 <140> CURRENT APPLICATION NUMBER: 10/691,165
12 <141> CURRENT FILING DATE: 2003-10-21
14 <150> PRIOR APPLICATION NUMBER: 09/689,486
15 <151> PRIOR FILING DATE: 2000-10-12
17 <150> PRIOR APPLICATION NUMBER: 60/159,805
18 <151> PRIOR FILING DATE: 1999-10-15
20 <150> PRIOR APPLICATION NUMBER: 60/159,992
21 <151> PRIOR FILING DATE: 1999-10-18
23 <150> PRIOR APPLICATION NUMBER: 60/160,952
24 <151> PRIOR FILING DATE: 1999-10-22
26 <160> NUMBER OF SEQ ID NOS: 64
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 430
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (61)..(234)
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42 atg gca gac aaa cca gac ata ggg gaa atc gcc agc ttc aat aag gcc 108
43 Met Ala Asp Lys Pro Asp Ile Gly Glu Ile Ala Ser Phe Asn Lys Ala
44 1 5 10 15
46 aag ctg aag aaa aca gag atg cag gag aac acc ctg ctg acc aaa gag 156
47 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
48 20 25 30
50 gcc att gag cag gag aag cgg gtg aaa ttt cct aag agc ctg gag gat 204
51 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
52 35 40 45
54 tcc cta ccc ctg tca tct tcg aga ccc cag tagtaatgtg gaggaagaat 254
55 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
56 50 55
58 caccacaaga tggacacaag ccacaaactg tgacgtgaac ctgggcactc cgtgctgatg 314
60 ccaccagcct gagggtcct atgggtccaa tcagactgcc aaattctctg gtttgccctg 374
62 ggatattata gaaaattatt tgcgtgaata atgaaaacac agctcatggc aaaaaa 430
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 58

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67 <212> TYPE: PRT
68 <213> ORGANISM: Homo sapiens
70 <400> SEQUENCE: 2
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72   1               5               10               15
74 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
75               20               25               30
77 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
78               35               40               45
80 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
81   50               55
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 13
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
90 <400> SEQUENCE: 3
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92   1               5               10
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96 <211> LENGTH: 3018
97 <212> TYPE: DNA
98 <213> ORGANISM: Homo sapiens
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102 gcggccacct gcgtgtccgc ggcgcgcggc gaagtgaatt tgctggacac gtcgaccatc 120
103 cacggggact ggggctggct cacgtatccg gctcatgggt gggactccat caacgagggtg 180
104 gacgagtcct tccagcccat ccacacgtac caggtttgca acgtcatgag ccccaaccag 240
105 aacaactggc tgcgcacgag ctgggtcccc cgagacggcg cccggcgcgct ctatgctgag 300
106 atcaagttta ccctgcgcga ctgcaacagc atgcctgggt tgctgggcac ctgcaaggag 360
107 accttcaacc tctactacct ggagtcggac cgcgacctgg gggccagcac acaagaaagc 420
108 cagttcctca aaatcgacac cattgcggcc gacgagagct tcacaggtgc cgaccttggt 480
109 gtgcggcgct tcaagctcaa cacggagggt cgcagtgtgg gtccccctag caagcgcggc 540
110 ttctacctgg ccttccagga catagggtgc tgccctggcca tcctctctct ccgcattctac 600
111 tataagaagt gccctgccat ggtgcgcaat ctggctgcct tctcggaggc agtgacgggg 660
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113 gacacaccca agatgtactg cagcgcgagg ggcgagtggc tcgtgcccat cggcaaattgc 780
114 gtgtgcagtg ccggctacga ggagcggcgg gatgcctgtg tggcctgtga gctgggcttc 840
115 tacaagtcag cccctgggga ccagctgtgt gcccgtgccc ctccccacag ccaactccga 900
116 gctccagccg cccaagcctg ccactgtgac ctacgtact accgtgcagc cctggacccg 960
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119 acctacaatg ccgtgtgccc ccgtgcccc tgggcactga gccgtgcga ggcattgtgg 1140
120 agcggcaccc gctttgtgcc ccagcagaca agcctggtgc aggcagcct gctgggtggc 1200
121 aacctgctgg ccacatgaa ctactccttc tggatcgagg ccgtcaatgg cgtgtccgac 1260
122 ctgagccccg agccccgcgg ggccgctgtg gtcaacatca ccacgaacca ggcagccccg 1320
123 tcccagggtg tggatgaccc tcaagagcgg gcggggcaga ccagcgtctc gctgctgtgg 1380
124 caggagcccc agcagccgaa cggcatcatc ctggagtatg agatcaagta ctacgagaag 1440
125 gacaaggaga tgcagagcta ctccaccctc aaggccgtca ccaccagagc caccgtctcc 1500
126 ggcctcaagc cgggcacccg ctacgtgttc cagggtccgag cccgcacctc agcaggctgt 1560

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127 ggccgcttca gccaggccat ggaggtggag accgggaaac cccggccccg ctatgacacc 1620
128 aggaccattg tctggatctg cctgacgctc atcacgggcc tgggtggtgct tctgctcctg 1680
129 ctcattctgca agaagaggca ctgtggctac agcaaggcct tccaggactc ggacgaggag 1740
130 aagatgcact atcagaatgg acaggcacc cccactgtct tccctgctct gcatcaccac 1800
131 cccgggaaagc tcccagagcc ccagttctat gcggaacccc acacctacga ggagccaggc 1860
132 cgggcggggcc gcagtttcac tcgggagatc gaggcctcta ggatccacat cgagaaaatc 1920
133 atcggctctg gagactccgg ggaagtctgc tacgggaggc tgcgggtgcc agggcagcgg 1980
134 gatgtgcccc tggccatcaa ggccctcaaa gccggctaca cggagagaca gaggcggggac 2040
135 ttcctgagcg aggcgtccat catggggcaa ttcgaccatc ccaacatcat ccgcctcgag 2100
136 ggtgtcgtca cccgtggccg cctggcaatg attgtgactg agtacatgga gaacggctct 2160
137 ctggacacct tcctgaggac ccacgacggg cagttcacca tcatgcagct ggtgggcatg 2220
138 ctgagaggag tgggtgcccg catgcgtac ctctcagacc tgggctatgt ccaccgagac 2280
139 ctggccgccc gcaacgtcct ggttgacagc aacctggtct gcaagggtgc tgacttcggg 2340
140 ctctcacggg tgctggagga cgaccgggat gctgcctaca ccaccacggg cgggaagatc 2400
141 cccatccgct ggacggcccc agaggccatc gccttcgca ccttctctc ggccagcgac 2460
142 gtgtggagct tcggcgtggt catgtgggag gtgctggcct atggggagcg gccctactgg 2520
143 aacatgacca accgggatgt gatcagctct gtggaggagg ggtaccgcct gcccgacccc 2580
144 atgggctgcc cccacgcctt gcaccagctc atgctcgact gttggcacia ggaccgggcg 2640
145 cagcggcctc gcttctccca gattgtcagt gtccctcgat cgctcatccg cagccctgag 2700
146 agtctcaggg ccaccgccac agtcagcagg tgcacacccc ctgccttcgt ccggagctgc 2760
147 tttgacctcc gagggggcag cgggtggcgt gggggcctca ccgtggggga ctggctggac 2820
148 tccatccgca tgggcccgtta ccgagaccac ttcgctgcgg gcggatactc ctctctgggc 2880
149 atggtgctac gcatgaacgc ccaggacgtg cgcgcctgg gcatcacct catgggccac 2940
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151 ccccgccggc acctctga                                     3018
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155 <211> LENGTH: 992
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 5
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161 1 5 10 15
163 Ala Ala Ala Ala Ala Thr Cys Val Ser Ala Ala Arg Gly Glu Val
164 20 25 30
166 Asn Leu Leu Asp Thr Ser Thr Ile His Gly Asp Trp Gly Trp Leu Thr
167 35 40 45
169 Tyr Pro Ala His Gly Trp Asp Ser Ile Asn Glu Val Asp Glu Ser Phe
170 50 55 60
172 Gln Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Ser Pro Asn Gln
173 65 70 75 80
175 Asn Asn Trp Leu Arg Thr Ser Trp Val Pro Arg Asp Gly Ala Arg Arg
176 85 90 95
178 Val Tyr Ala Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Met Pro
179 100 105 110
181 Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Leu Glu
182 115 120 125
184 Ser Asp Arg Asp Leu Gly Ala Ser Thr Gln Glu Ser Gln Phe Leu Lys
185 130 135 140
187 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gly Ala Asp Leu Gly

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188 145          150          155          160
190 Val Arg Arg Leu Lys Leu Asn Thr Glu Val Arg Ser Val Gly Pro Leu
191          165          170          175
193 Ser Lys Arg Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Leu
194          180          185          190
196 Ala Ile Leu Ser Leu Arg Ile Tyr Tyr Lys Lys Cys Pro Ala Met Val
197          195          200          205
199 Arg Asn Leu Ala Ala Phe Ser Glu Ala Val Thr Gly Ala Asp Ser Ser
200          210          215          220
202 Ser Leu Val Glu Val Arg Gly Gln Cys Val Arg His Ser Glu Glu Arg
203 225          230          235          240
205 Asp Thr Pro Lys Met Tyr Cys Ser Ala Glu Gly Glu Trp Leu Val Pro
206          245          250          255
208 Ile Gly Lys Cys Val Cys Ser Ala Gly Tyr Glu Glu Arg Arg Asp Ala
209          260          265          270
211 Cys Val Ala Cys Glu Leu Gly Phe Tyr Lys Ser Ala Pro Gly Asp Gln
212          275          280          285
214 Leu Cys Ala Arg Cys Pro Pro His Ser His Ser Ala Ala Pro Ala Ala
215          290          295          300
217 Gln Ala Cys His Cys Asp Leu Ser Tyr Tyr Arg Ala Ala Leu Asp Pro
218 305          310          315          320
220 Pro Ser Ser Ala Cys Thr Arg Pro Pro Ser Ala Pro Val Asn Leu Ile
221          325          330          335
223 Ser Ser Val Asn Gly Thr Ser Val Thr Leu Glu Trp Ala Pro Pro Leu
224          340          345          350
226 Asp Pro Gly Gly Arg Ser Asp Ile Thr Tyr Asn Ala Val Cys Arg Arg
227          355          360          365
229 Cys Pro Trp Ala Leu Ser Arg Cys Glu Ala Cys Gly Ser Gly Thr Arg
230          370          375          380
232 Phe Val Pro Gln Gln Thr Ser Leu Val Gln Ala Ser Leu Leu Val Ala
233 385          390          395          400
235 Asn Leu Leu Ala His Met Asn Tyr Ser Phe Trp Ile Glu Ala Val Asn
236          405          410          415
238 Gly Val Ser Asp Leu Ser Pro Glu Pro Arg Arg Ala Ala Val Val Asn
239          420          425          430
241 Ile Thr Thr Asn Gln Ala Ala Pro Ser Gln Val Val Val Ile Arg Gln
242          435          440          445
244 Glu Arg Ala Gly Gln Thr Ser Val Ser Leu Leu Trp Gln Glu Pro Glu
245          450          455          460
247 Gln Pro Asn Gly Ile Ile Leu Glu Tyr Glu Ile Lys Tyr Tyr Glu Lys
248 465          470          475          480
250 Asp Lys Glu Met Gln Ser Tyr Ser Thr Leu Lys Ala Val Thr Thr Arg
251          485          490          495
253 Ala Thr Val Ser Gly Leu Lys Pro Gly Thr Arg Tyr Val Phe Gln Val
254          500          505          510
256 Arg Ala Arg Thr Ser Ala Gly Cys Gly Arg Phe Ser Gln Ala Met Glu
257          515          520          525
259 Val Glu Thr Gly Lys Pro Arg Pro Arg Tyr Asp Thr Arg Thr Ile Val
260          530          535          540

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262 Trp Ile Cys Leu Thr Leu Ile Thr Gly Leu Val Val Leu Leu Leu Leu
263 545                    550                    555                    560
265 Leu Ile Cys Lys Lys Arg His Cys Gly Tyr Ser Lys Ala Phe Gln Asp
266                    565                    570                    575
268 Ser Asp Glu Glu Lys Met His Tyr Gln Asn Gly Gln Ala Pro Pro Pro
269                    580                    585                    590
271 Val Phe Leu Pro Leu His His Pro Pro Gly Lys Leu Pro Glu Pro Gln
272                    595                    600                    605
274 Phe Tyr Ala Glu Pro His Thr Tyr Glu Glu Pro Gly Arg Ala Gly Arg
275                    610                    615                    620
277 Ser Phe Thr Arg Glu Ile Glu Ala Ser Arg Ile His Ile Glu Lys Ile
278 625                    630                    635                    640
280 Ile Gly Ser Gly Asp Ser Gly Glu Val Cys Tyr Gly Arg Leu Arg Val
281                    645                    650                    655
283 Pro Gly Gln Arg Asp Val Pro Val Ala Ile Lys Ala Leu Lys Ala Gly
284                    660                    665                    670
286 Tyr Thr Glu Arg Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met
287                    675                    680                    685
289 Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr
290                    690                    695                    700
292 Arg Gly Arg Leu Ala Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser
293 705                    710                    715                    720
295 Leu Asp Thr Phe Leu Arg Thr His Asp Gly Gln Phe Thr Ile Met Gln
296                    725                    730                    735
298 Leu Val Gly Met Leu Arg Gly Val Gly Ala Gly Met Arg Tyr Leu Ser
299                    740                    745                    750
301 Asp Leu Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
302                    755                    760                    765
304 Asp Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val
305                    770                    775                    780
307 Leu Glu Asp Asp Pro Asp Ala Ala Tyr Thr Thr Thr Gly Gly Lys Ile
308 785                    790                    795                    800
310 Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Thr Phe Ser
311                    805                    810                    815
313 Ser Ala Ser Asp Val Trp Ser Phe Gly Val Val Met Trp Glu Val Leu
314                    820                    825                    830
316 Ala Tyr Gly Glu Arg Pro Tyr Trp Asn Met Thr Asn Arg Asp Val Ile
317                    835                    840                    845
319 Ser Ser Val Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Gly Cys Pro
320                    850                    855                    860
322 His Ala Leu His Gln Leu Met Leu Asp Cys Trp His Lys Asp Arg Ala
323 865                    870                    875                    880
325 Gln Arg Pro Arg Phe Ser Gln Ile Val Ser Val Leu Asp Ala Leu Ile
326                    885                    890                    895
328 Arg Ser Pro Glu Ser Leu Arg Ala Thr Ala Thr Val Ser Arg Cys Pro
329                    900                    905                    910
331 Pro Pro Ala Phe Val Arg Ser Cys Phe Asp Leu Arg Gly Gly Ser Gly
332                    915                    920                    925
334 Gly Gly Gly Gly Leu Thr Val Gly Asp Trp Leu Asp Ser Ile Arg Met

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**VERIFICATION SUMMARY**

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